

RAW SEQUENCE LISTING

DATE: 05/25/2000

PATENT APPLICATION: US/09/388,221A

TIME: 15:49:41

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Output Set : N:\CRF3\05252000\I388221A.raw

3 <110> APPLICANT: Reed, John C.
5 <120> TITLE OF INVENTION: Novel Card Proteins Involved in Cell Death Regulation
7 <130> FILE REFERENCE: P-LJ 3650
9 <140> CURRENT APPLICATION NUMBER: 09/388,221A
10 <141> CURRENT FILING DATE: 1999-09-01
12 <160> NUMBER OF SEQ ID NOS: 18
14 <170> SOFTWARE: PatentIn Ver. 2.1
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 4422
18 <212> TYPE: DNA
19 <213> ORGANISM: Homo sapiens
21 <220> FEATURE:
22 <221> NAME/KEY: CDS
23 <222> LOCATION: (1)..(4422)
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28 1 5 10 15
30 aag aag gag gag ctg aag gag ttc cag ctt ctg ctc gcc aat aaa gcg 96
31 Lys Lys Glu Glu Leu Lys Glu Phe Gln Leu Leu Leu Ala Asn Lys Ala
32 20 25 30
34 cac tcc agg agc tct tgg ggt gag aca ccc gct cag cca gag aag acg 144
35 His Ser Arg Ser Ser Ser Gly Glu Thr Pro Ala Gln Pro Glu Lys Thr
36 35 40 45
38 agt ggc atg gag gtg gcc tgg tac ctg gtg gct cag tat ggg gag cag 192
39 Ser Gly Met Glu Val Ala Ser Tyr Leu Val Ala Gln Tyr Gly Glu Gln
40 50 55 60
42 cgg gcc tgg gac cta gcc ctc cat acc tgg gag cag atg ggg ctg agg 240
43 Arg Ala Trp Asp Leu Ala Leu His Thr Trp Glu Gln Met Gly Leu Arg
44 65 70 75 80
46 tca ctg tgc gcc caa gcc cag gaa ggg gca ggc cac tct ccc tca ttc 288
47 Ser Leu Cys Ala Gln Ala Gln Glu Gly Ala Gly His Ser Pro Ser Phe
48 85 90 95
50 ccc tac agc cca agt gaa ccc cac ctg ggg tct ccc agc caa ccc acc 336
51 Pro Tyr Ser Pro Ser Glu Pro His Leu Gly Ser Pro Ser Gln Pro Thr
52 100 105 110
54 tcc acc gca gtg cta atg ccc tgg atc cat gaa ttg ccg gcg ggg tgc 384
55 Ser Thr Ala Val Leu Met Pro Trp Ile His Glu Leu Pro Ala Gly Cys
56 115 120 125
58 acc cag ggc tca gag aga agg gtt ttg aga cag ctg cct gac aca tct 432
59 Thr Gln Gly Ser Glu Arg Arg Val Leu Arg Gln Leu Pro Asp Thr Ser
60 130 135 140
62 gga cgc cgc tgg aga gaa atc tct gcc tca ctc ctc tac caa gct ctt 480
63 Gly Arg Arg Trp Arg Glu Ile Ser Ala Ser Leu Leu Tyr Gln Ala Leu
64 145 150 155 160
66 cca agc tcc cca gac cat gag tct cca agc cag gag tca ccc aac gcc 528
67 Pro Ser Ser Pro Asp His Glu Ser Pro Ser Gln Glu Ser Pro Asn Ala

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70 ccc aca tcc aca gca gtg ctg ggg agc tgg gga tcc cca cct cag ccc 576
71 Pro Thr Ser Thr Ala Val Leu Gly Ser Trp Gly Ser Pro Pro Gln Pro
72                               180                               185                               190
74 agc cta gca ccc aga gag cag gag gct cct ggg acc caa tgg cct ctg 624
75 Ser Leu Ala Pro Arg Glu Gln Glu Ala Pro Gly Thr Gln Trp Pro Leu
76                               195                               200                               205
78 gat gaa acg tca gga att tac tac aca gaa atc aga gaa aga gag aga 672
79 Asp Glu Thr Ser Gly Ile Tyr Tyr Thr Glu Ile Arg Glu Arg Glu Arg
80                               210                               215                               220
82 gag aaa tca gag aaa ggc agg ccc cca tgg gca gcg gtg gta gga acg 720
83 Glu Lys Ser Glu Lys Gly Arg Pro Pro Trp Ala Ala Val Val Gly Thr
84 225                               230                               235                               240
86 ccc cca cag gcg cac acc agc cta cag ccc cac cac cca tgg gag 768
87 Pro Pro Gln Ala His Thr Ser Leu Gln Pro His His His Pro Trp Glu
88                               245                               250                               255
90 cct tct gtg aga gag agc ctc tgt tcc aca tgg ccc tgg aaa aat gag 816
91 Pro Ser Val Arg Glu Ser Leu Cys Ser Thr Trp Pro Trp Lys Asn Glu
92                               260                               265                               270
94 gat ttt aac caa aaa ttc aca cag ctg cta ctt cta caa aga cct cac 864
95 Asp Phe Asn Gln Lys Phe Thr Gln Leu Leu Leu Leu Gln Arg Pro His
96                               275                               280                               285
98 ccc aga agc caa gat ccc ctg gtc aag aga agc tgg cct gat tat gtg 912
99 Pro Arg Ser Gln Asp Pro Leu Val Lys Arg Ser Trp Pro Asp Tyr Val
100                               290                               295                               300
102 gag gag aat cga gga cat tta att gag atc aga gac tta ttt ggc cca 960
103 Glu Glu Asn Arg Gly His Leu Ile Glu Ile Arg Asp Leu Phe Gly Pro
104 305                               310                               315                               320
106 ggc ctg gat acc caa gaa cct cgc ata gtc ata ctg cag ggg gct gct 1008
107 Gly Leu Asp Thr Gln Glu Pro Arg Ile Val Ile Leu Gln Gly Ala Ala
108                               325                               330                               335
110 gga att ggg aag tca aca ctg gcc agg cag gtg aag gaa gcc tgg ggg 1056
111 Gly Ile Gly Lys Ser Thr Leu Ala Arg Gln Val Lys Glu Ala Trp Gly
112                               340                               345                               350
114 aga ggc cag ctg tat ggg gac cgc ttc cag cat gtc ttc tac ttc agc 1104
115 Arg Gly Gln Leu Tyr Gly Asp Arg Phe Gln His Val Phe Tyr Phe Ser
116                               355                               360                               365
118 tgc aga gag ctg gcc cag tcc aag gtg gtg agt ctc gct gag ctc atc 1152
119 Cys Arg Glu Leu Ala Gln Ser Lys Val Val Ser Leu Ala Glu Leu Ile
120                               370                               375                               380
122 gga aaa gat ggg aca gcc act ccg gct ccc att aga cag atc ctg tct 1200
123 Gly Lys Asp Gly Thr Ala Thr Pro Ala Pro Ile Arg Gln Ile Leu Ser
124 385                               390                               395                               400
126 agg cca gag cgg ctg ctc ttc atc ctc gat ggt gta gat gag cca gga 1248
127 Arg Pro Glu Arg Leu Leu Phe Ile Leu Asp Gly Val Asp Glu Pro Gly
128                               405                               410                               415
130 tgg gtc ttg cag gag ccg agt tct gag ctc tgt ctg cac tgg agc cag 1296
131 Trp Val Leu Gln Glu Pro Ser Ser Glu Leu Cys Leu His Trp Ser Gln
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136			435					440					445				
138	ctt	ccc	gag	gca	tcc	ttc	ctg	atc	acg	gct	cgg	acc	aca	gct	ctg	cag	1392
139	Leu	Pro	Glu	Ala	Ser	Phe	Leu	Ile	Thr	Ala	Arg	Thr	Thr	Ala	Leu	Gln	
140		450					455					460					
142	aac	ctc	att	cct	tct	ttg	gag	gca	cgt	tgg	gta	gag	gtc	ctg	ggg		1440
143	Asn	Leu	Ile	Pro	Ser	Leu	Glu	Gln	Ala	Arg	Trp	Val	Glu	Val	Leu	Gly	
144	465					470				475					480		
146	ttc	tct	gag	tcc	agc	agg	aag	gaa	tat	ttc	tac	aga	tat	ttc	aca	gat	1488
147	Phe	Ser	Glu	Ser	Ser	Arg	Lys	Glu	Tyr	Phe	Tyr	Arg	Tyr	Phe	Thr	Asp	
148				485						490				495			
150	gaa	agg	caa	gca	att	aga	gcc	ttt	agg	ttg	gtc	aaa	tca	aac	aaa	gag	1536
151	Glu	Arg	Gln	Ala	Ile	Arg	Ala	Phe	Arg	Leu	Val	Lys	Ser	Asn	Lys	Glu	
152			500					505					510				
154	ctc	tgg	gcc	ctg	tgt	ctt	gtg	ccc	tgg	gtg	tcc	tgg	ctg	gcc	tgc	act	1584
155	Leu	Trp	Ala	Leu	Cys	Leu	Val	Pro	Trp	Val	Ser	Trp	Leu	Ala	Cys	Thr	
156		515					520					525					
158	tgc	ctg	atg	cag	cag	atg	aag	cgg	aag	gaa	aaa	ctc	aca	ctg	act	tcc	1632
159	Cys	Leu	Met	Gln	Gln	Met	Lys	Arg	Lys	Glu	Lys	Leu	Thr	Leu	Thr	Ser	
160		530				535						540					
162	aag	acc	acc	aca	acc	ctc	tgt	cta	cat	tac	ctt	gcc	cag	gct	ctc	caa	1680
163	Lys	Thr	Thr	Thr	Thr	Leu	Cys	Leu	His	Tyr	Leu	Ala	Gln	Ala	Leu	Gln	
164	545					550				555					560		
166	gct	cag	cca	ttg	gga	ccc	cag	ctc	aga	gac	ctc	tgc	tct	ctg	gct	gct	1728
167	Ala	Gln	Pro	Leu	Gly	Pro	Gln	Leu	Arg	Asp	Leu	Cys	Ser	Leu	Ala	Ala	
168				565				570					575				
170	gag	ggc	atc	tgg	caa	aaa	aag	acc	ctt	ttc	agt	cca	gat	gac	ctc	agg	1776
171	Glu	Gly	Ile	Trp	Gln	Lys	Lys	Thr	Leu	Phe	Ser	Pro	Asp	Asp	Leu	Arg	
172			580					585					590				
174	aag	cat	ggg	tta	gat	ggg	gcc	atc	atc	tcc	acc	ttc	ttg	aag	atg	ggt	1824
175	Lys	His	Gly	Leu	Asp	Gly	Ala	Ile	Ser	Thr	Phe	Leu	Lys	Met	Gly		
176		595				600						605					
178	att	ctt	caa	gag	cac	ccc	atc	cct	ctg	agc	tac	agc	ttc	att	cac	ctc	1872
179	Ile	Leu	Gln	Glu	His	Pro	Ile	Pro	Leu	Ser	Tyr	Ser	Phe	Ile	His	Leu	
180		610				615						620					
182	tgt	ttc	caa	gag	ttc	ttt	gca	gca	atg	tcc	tat	gtc	ttg	gag	gat	gag	1920
183	Cys	Phe	Gln	Glu	Phe	Phe	Ala	Ala	Met	Ser	Tyr	Val	Leu	Glu	Asp	Glu	
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186	aag	ggg	aga	ggt	aaa	cat	tct	aat	tgc	atc	ata	gat	ttg	gaa	aag	acg	1968
187	Lys	Gly	Arg	Gly	Lys	His	Ser	Asn	Cys	Ile	Ile	Asp	Leu	Glu	Lys	Thr	
188				645						650					655		
190	cta	gaa	gca	tat	gga	ata	cat	ggc	ctg	ttt	ggg	gca	tca	acc	aca	cgt	2016
191	Leu	Glu	Ala	Tyr	Gly	Ile	His	Gly	Leu	Phe	Gly	Ala	Ser	Thr	Thr	Arg	
192			660					665					670				
194	ttc	cta	ttg	ggc	ctg	tta	agt	gat	gag	ggg	gag	aga	gag	atg	gag	aac	2064
195	Phe	Leu	Leu	Gly	Leu	Leu	Ser	Asp	Glu	Gly	Glu	Arg	Glu	Met	Glu	Asn	
196		675				680						685					
198	atc	ttt	cac	tgc	cgg	ctg	tct	cag	ggg	agg	aac	ctg	atg	cag	tgg	gtc	2112

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203	Pro	Ser	Leu	Gln	Leu	Leu	Gln	Pro	His	Ser	Leu	Glu	Ser	Leu	His		
204	705					710				715					720		
206	tgc	ttg	tac	gag	act	cgg	aac	aaa	acg	ttc	ctg	aca	caa	gtg	atg	gcc	2208
207	Cys	Leu	Tyr	Glu	Thr	Arg	Asn	Lys	Thr	Phe	Leu	Thr	Gln	Val	Met	Ala	
208					725					730					735		
210	cat	ttc	gaa	gaa	atg	ggc	atg	tgt	gta	gaa	aca	gac	atg	gag	ctc	tta	2256
211	His	Phe	Glu	Glu	Met	Gly	Met	Cys	Val	Glu	Thr	Asp	Met	Glu	Leu	Leu	
212				740					745					750			
214	gtg	tgc	act	ttc	tgc	att	aaa	ttc	agc	cgc	cac	gtg	aag	aag	ctt	cag	2304
215	Val	Cys	Thr	Phe	Cys	Ile	Lys	Phe	Ser	Arg	His	Val	Lys	Lys	Leu	Gln	
216			755					760					765				
218	ctg	att	gag	ggc	agg	cag	cac	aga	tca	aca	tgg	agc	ccc	acc	atg	gta	2352
219	Leu	Ile	Glu	Gly	Arg	Gln	His	Arg	Ser	Thr	Trp	Ser	Pro	Thr	Met	Val	
220		770				775						780					
222	gtc	ctg	ttc	agg	tgg	gtc	cca	gtc	aca	gat	gcc	tat	tgg	cag	att	ctc	2400
223	Val	Leu	Phe	Arg	Trp	Val	Pro	Val	Thr	Asp	Ala	Tyr	Trp	Gln	Ile	Leu	
224	785					790					795					800	
226	ttc	tcc	gtc	ctc	aag	gtc	acc	aga	aac	ctg	aag	gag	ctg	gac	cta	agt	2448
227	Phe	Ser	Val	Leu	Lys	Val	Thr	Arg	Asn	Leu	Lys	Glu	Leu	Asp	Leu	Ser	
228				805						810					815		
230	gga	aac	tgc	ctg	agc	cac	tct	gca	gtg	aag	agt	ctt	tgt	aag	acc	ctg	2496
231	Gly	Asn	Ser	Leu	Ser	His	Ser	Ala	Val	Lys	Ser	Leu	Cys	Lys	Thr	Leu	
232				820					825					830			
234	aga	cgc	cct	cgc	tgc	ctc	ctg	gag	acc	ctg	cgg	ttg	gct	ggc	tgt	ggc	2544
235	Arg	Arg	Pro	Arg	Cys	Leu	Leu	Glu	Thr	Leu	Arg	Leu	Ala	Gly	Cys	Gly	
236			835					840					845				
238	ctc	aca	gct	gag	gac	tgc	aag	gac	ctt	gcc	ttt	ggg	ctg	aga	gcc	aac	2592
239	Leu	Thr	Ala	Glu	Asp	Cys	Lys	Asp	Leu	Ala	Phe	Gly	Leu	Arg	Ala	Asn	
240		850				855					860						
242	cag	acc	ctg	acc	gag	ctg	gac	ctg	agc	ttc	aat	gtg	ctc	acg	gat	gct	2640
243	Gln	Thr	Leu	Thr	Glu	Leu	Asp	Leu	Ser	Phe	Asn	Val	Leu	Thr	Asp	Ala	
244	865					870					875					880	
246	gga	gcc	aaa	cac	ctt	tgc	cag	aga	ctg	aga	cag	ccg	agc	tgc	aag	cta	2688
247	Gly	Ala	Lys	His	Leu	Cys	Gln	Arg	Leu	Arg	Gln	Pro	Ser	Cys	Lys	Leu	
248				885						890					895		
250	cag	cga	ctg	cag	ctg	gtc	agc	tgt	ggc	ctc	acg	tct	gac	tgc	tgc	cag	2736
251	Gln	Arg	Leu	Gln	Leu	Val	Ser	Cys	Gly	Leu	Thr	Ser	Asp	Cys	Cys	Gln	
252			900						905					910			
254	gac	ctg	gcc	tct	gtg	ctt	agt	gcc	agc	ccc	agc	ctg	aag	gag	cta	gac	2784
255	Asp	Leu	Ala	Ser	Val	Leu	Ser	Ala	Ser	Pro	Ser	Leu	Lys	Glu	Leu	Asp	
256			915					920					925				
258	ctg	cag	cag	aac	aac	ctg	gat	gac	gtt	ggc	gtg	cga	ctg	ctc	tgt	gag	2832
259	Leu	Gln	Gln	Asn	Asn	Leu	Asp	Asp	Val	Gly	Val	Arg	Leu	Leu	Cys	Glu	
260		930						935					940				
262	ggg	ctc	agg	cat	cct	gcc	tgc	aaa	ctc	ata	cgc	ctg	ggg	ctg	gac	cag	2880
263	Gly	Leu	Arg	His	Pro	Ala	Cys	Lys	Leu	Ile	Arg	Leu	Gly	Leu	Asp	Gln	

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268          965          970          975
270 gag aaa cct cag ctg ctc atc ttc agc aga cgg aaa cca agt gtg atg 2976
271 Glu Lys Pro Gln Leu Leu Ile Phe Ser Arg Arg Lys Pro Ser Val Met
272          980          985          990
274 acc cct act gag ggc ctg gat acg gga gag atg agt aat agc aca tcc 3024
275 Thr Pro Thr Glu Gly Leu Asp Thr Gly Glu Met Ser Asn Ser Thr Ser
276          995          1000          1005
278 tca ctc aag cgg cag aga ctc gga tca gag agg gcg gct tcc cat gtt 3072
279 Ser Leu Lys Arg Gln Arg Leu Gly Ser Glu Arg Ala Ala Ser His Val
280          1010          1015          1020
282 gct cag gct aat ctc aaa ctc ctg gac gtg agc aag atc ttc cca att 3120
283 Ala Gln Ala Asn Leu Lys Leu Leu Asp Val Ser Lys Ile Phe Pro Ile
284          1025          1030          1035          1040
286 gct gag att gca gag gaa agc tcc cca gag gta gta ccg gtg gaa ctc 3168
287 Ala Glu Ile Ala Glu Glu Ser Ser Pro Glu Val Val Pro Val Glu Leu
288          1045          1050          1055
290 ttg tgc gtg cct tct cct gcc tct caa ggg gac ctg cat acg aag cct 3216
291 Leu Cys Val Pro Ser Pro Ala Ser Gln Gly Asp Leu His Thr Lys Pro
292          1060          1065          1070
294 ttg ggg act gac gat gac ttc tgg ggc ccc acg ggg cct gtg gct act 3264
295 Leu Gly Thr Asp Asp Phe Trp Gly Pro Thr Gly Pro Val Ala Thr
296          1075          1080          1085
298 gag gta gtt gac aaa gaa aag aac ttg tac cga gtt cac ttc cct gta 3312
299 Glu Val Val Asp Lys Glu Lys Asn Leu Tyr Arg Val His Phe Pro Val
300          1090          1095          1100
302 gct ggc tcc tac cgc tgg ccc aac acg ggt ctc tgc ttt gtg atg aga 3360
303 Ala Gly Ser Tyr Arg Trp Pro Asn Thr Gly Leu Cys Phe Val Met Arg
304          1105          1110          1115          1120
306 gaa gcg gtg acc gtt gag att gaa ttc tgt gtg tgg gac cag ttc ctg 3408
307 Glu Ala Val Thr Val Glu Ile Glu Phe Cys Val Trp Asp Gln Phe Leu
308          1125          1130          1135
310 ggt gag atc aac cca cag cac agc tgg atg gtg gca ggg cct ctg ctg 3456
311 Gly Glu Ile Asn Pro Gln His Ser Trp Met Val Ala Gly Pro Leu Leu
312          1140          1145          1150
314 gac atc aag gct gag cct gga gct gtg gaa gct gtg cac ctc cct cac 3504
315 Asp Ile Lys Ala Glu Pro Gly Ala Val Glu Ala Val His Leu Pro His
316          1155          1160          1165
318 ttt gtg gct ctc caa ggg ggc cat gtg gac aca tcc ctg ttc caa atg 3552
319 Phe Val Ala Leu Gln Gly Gly His Val Asp Thr Ser Leu Phe Gln Met
320          1170          1175          1180
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323 Ala His Phe Lys Glu Glu Gly Met Leu Leu Glu Lys Pro Ala Arg Val
324          1185          1190          1195          1200
326 gag ctg cat cac ata gtt ctg gaa aac ccc agc ttc tcc ccc ttg gga 3648
327 Glu Leu His His Ile Val Leu Glu Asn Pro Ser Phe Ser Pro Leu Gly
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L:3037 M:258 W: Mandatory Feature missing, <220> FEATURE: